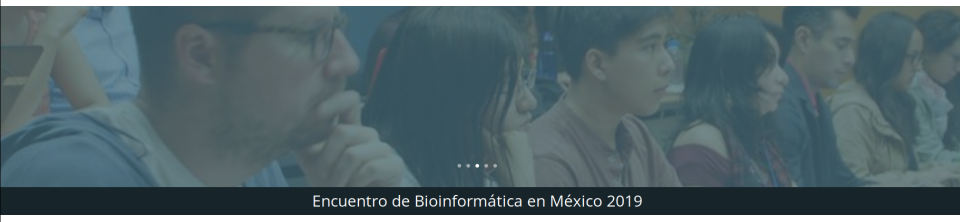
- TIB2019-T3 -
Análisis comparativo de genomas microbianos: Pangenómica y filoinformática



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Acceso al material del curso:
https://github.com/vinuesa/TIB-filoinfo

Sesión 8: Estima de filogenias genómicas con GET_PHYLOMARKERS

Frontiers In Microbiology Research Topics

frontiers

Research Topic

Microbial Taxonomy, Phylogeny and Biodiversity

Submission closed.

Overview | 18 Articles | 156 Authors | Impact | Comments

GET_PHYLOMARKERS, a Software Package to Select Optimal Orthologous Clusters for Phylogenomics and Inferring Pan-Genome Phylogenies, Used for a Critical Geno-Taxonomic Revision of the Genus Stenotrophomonas

Pablo Vinuesa , Luz E. Ochoa-Sánchez and Bruno Contreras-Moreira

Original Research The massive accumulation of genome-sequences in public databases promoted the proliferation of genome-level phylogenetic analyses in many areas of biological research. However, due to diverse evolutionary and genetic processes, many loci have ...

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https://github.com/vinuesa/get_phylomarkers

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get_phylomarkers
A pipeline to select optimal markers for microbial phylogenomics, population genetics and genomic taxonomy
Perl ★2 2

Pablo Vinuesa
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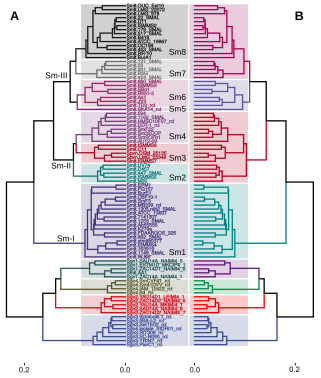
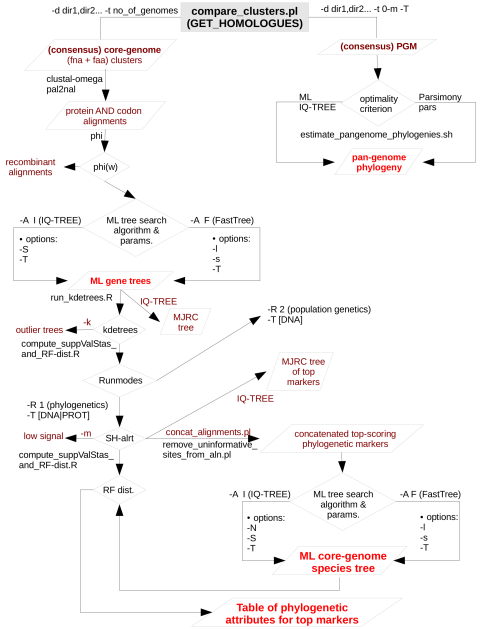


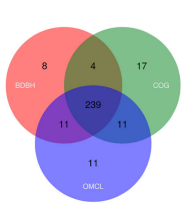
Flowchart showing how the GET_PHYLOMARKERS package integrates with GET_HOMOLOGUES

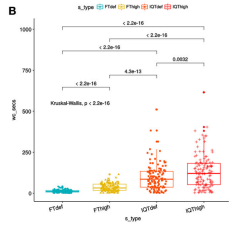


Vinuesa et al., 2018

Benchmark analyses of the phylogenetic performance of FT vs IQ-TREE

Consensus core-genome (n=239) computed with GET_HOMOLOGUES



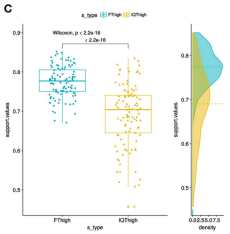


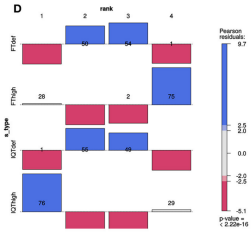
Computation time required by FT and IQT when run under "default" (FTdef, IQTdef) and thorough (FThigh, IQThigh) search modes (s_type) on the 239 consensus Clusters

Kruskal-Wallis $p < 2.2e-16$

Distribution of SH-alrt branch support values of gene-trees found by the FThigh and IQThigh Searches.

Wilcoxon signed-rank test $p < 2.2e-16$

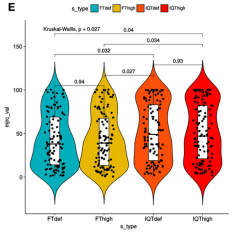


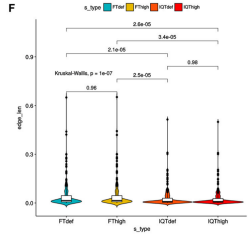


Association plot summarizing the results of **multi-way Chi-Square analyses of the ln*L* score ranks** (1–4, meaning best to worst) **of the 105 top-scoring ML gene-trees** passing the kdetrees filter in the IQThigh run (Table 2) for each search-type $p < 2.2e-16$

Distribution of **consensus values from majority-rule consensus trees** computed from the gene trees passing all the filters, as a function Of search-type.

Kruskal-Wallis $p < 0.027$



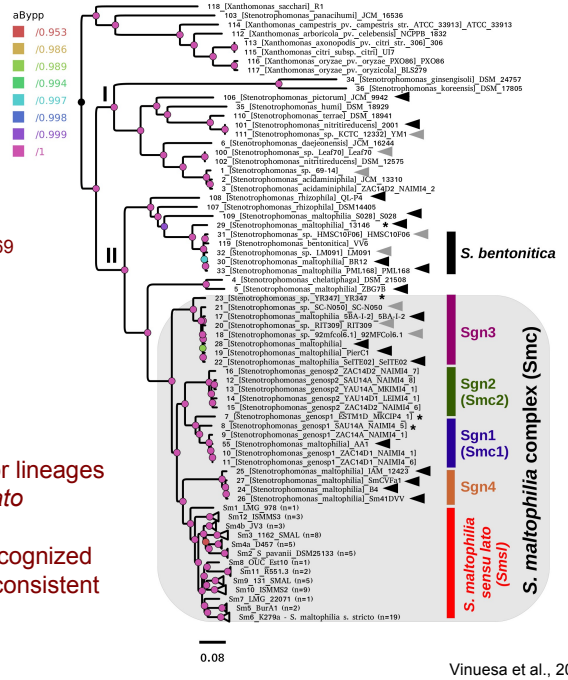


Distribution of the **edge-lengths of species-trees** Computed from the con-catenated top-scoring Markers, as a function of Search-type

Kruskal-Wallis $p < 1e-7$

ML species tree

- 118 genomes
- Top 52(/231) markers
- GTR+ASC+F+R7



→ ~8% misclassified genomes 13/169

→ ~8% unclassified genomes 14/169

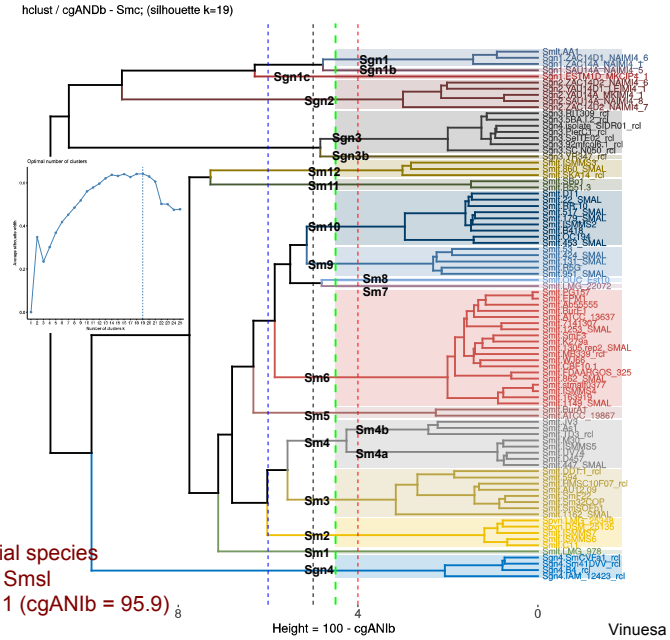
- reclassified 27 RefSeq genome sequences!

- The Smc is split into 5 major lineages including *S. maltophilia s. lato*

- 13 clades (species?) are recognized within the latter, which are consistent with a 95.9% cgANIb cutoff

Vinuesa et al., 2018

Unsupervised learning methods to find groups within the Smc and *S. maltophilia s. lato* lineages based on cgANDb (= 100 - cgANIb)



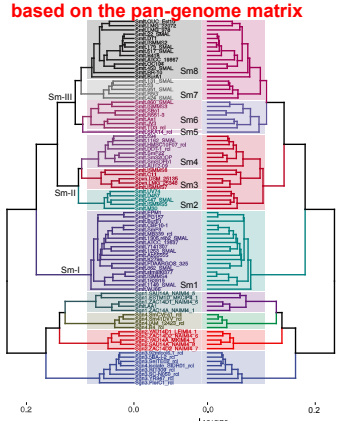
- up to 13 potential species resolved within Smsl at cgANDb = 4.1 (cgANIb = 95.9)

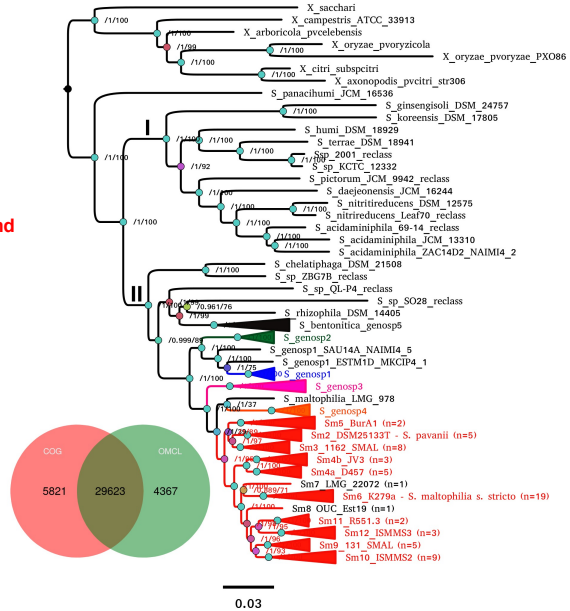
Vinuesa et al., 2018

ML pan-genome tree

- 118 genomes
- 29,623 markers
- GTR2+F0+R4

Unsupervised learning methods to find species-like clusters in the Smc based on the pan-genome matrix





Model	LnL	df	AIC	AICc	BIC
GTR2+FQ+R4	-322836.2380	242	646156.4760	646160.4791	648164.1821
MK+FQ+R2	-337220.7785	237	674915.5571	674919.3962	676881.7817

Vinuesa et al., 2018